

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number:

10/S37/102

Source:

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RAW SEQUENCE LISTING

DATE: 05/01/2006

PATENT APPLICATION: US/10/537,102

TIME: 11:01:26

Input Set : A:\2006-01-26 0933-0246PUS1.ST25.txt

Output Set : N:\CRF4\05012006\J537102.raw

3 <110> APPLICANT: Kuja-Panula, Juha
 4 Kiiltomaki, Marjaana
 5 Rauvala, Heikki
 7 <120> TITLE OF INVENTION: NOVEL PROTEIN AND USES THEREOF
 9 <130> FILE REFERENCE: 0933-0246PUS1
 11 <140> CURRENT APPLICATION NUMBER: US 10/537,102
 12 <141> CURRENT FILING DATE: 2005-06-02
 14 <150> PRIOR APPLICATION NUMBER: US 60/433,011
 15 <151> PRIOR FILING DATE: 2002-12-13
 17 <160> NUMBER OF SEQ ID NOS: 79
 19 <170> SOFTWARE: PatentIn version 3.3
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1479
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(1479)
 30 <400> SEQUENCE: 1

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33	1 5 10 15	
35	ttg tcc ctg ctg ctt ttt gag gtg gcc aga gct ggc cga gcc gtg gtt	96
36	Leu Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val	
37	20 25 30	
39	agc tgt cct gcc gcc tgc ttg tgc gcc agc aac atc ctc agc tgc tcc	144
40	Ser Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser	
41	35 40 45	
43	aag cag cag ctg ccc aat gtg ccc cat tcc ttg ccc agt tac aca gca	192
44	Lys Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala	
45	50 55 60	
47	cta ctg gac ctc agt cac aac aac ctg agc cgc ctg cgg gcc gag tgg	240
48	Leu Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp	
49	65 70 75 80	
51	acc ccc acg cgc ctg acc caa ctg cac tcc ctg ctg ctg agc cac aac	288
52	Thr Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn	
53	85 90 95	
55	cac ctg aac ttc atc tcc tct gag gcc ttt tcc ccg gta ccc aac ctg	336
56	His Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu	
57	100 105 110	
59	cgc tac ctg gac ctc tcc tcc aac cag ctg cgt aca ctg gat gag ttc	384
60	Arg Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe	
61	115 120 125	

(pg. 6)

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63 ctg ttc agt gac ctg caa gta ctg gag gtg ctg ctg ctc tac aat aac 432
64 Leu Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Tyr Asn Asn
65      130      135      140
67 cac atc atg gcg gtg gac cgg tgc gcc ttc gat gac atg gcc cag ctg 480
68 His Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu
69 145      150      155      160
71 cag aaa ctc tac ttg agc cag aac cag atc tct cgc ttc cct ctg gaa 528
72 Gln Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu
73      165      170      175
75 ctg gtc aag gaa gga gcc aag cta ccc aaa cta acg ctc ctg gat ctc 576
76 Leu Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu
77      180      185      190
79 tct tct aac aag ctg aag aac ttg cca ttg cct gac ctg cag aag ctg 624
80 Ser Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu
81      195      200      205
83 ccg gcc tgg atc aag aat ggg ctg tac cta cat aac aac ccc ctg aac 672
84 Pro Ala Trp Ile Lys Asn Gly Leu Tyr Leu His Asn Asn Pro Leu Asn
85      210      215      220
87 tgc gac tgt gag ctc tac cag ctg ttt tca cac tgg cag tat cgg cag 720
88 Cys Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln
89 225      230      235      240
91 ctg agc tcc gtg atg gac ttt caa gag gat ctg tac tgc atg aac tcc 768
92 Leu Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser
93      245      250      255
95 aag aag ctg cac aat gtc ttc aac ctg agt ttc ctc aac tgt ggc gag 816
96 Lys Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu
97      260      265      270
99 tac aag gag cgt gcc tgg gag gcc cac ctg ggt gac acc ttg atc atc 864
100 Tyr Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile
101      275      280      285
103 aag tgt gac acc aag cag caa ggg atg acc aag gtg tgg gtg aca cca 912
104 Lys Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro
105      290      295      300
107 agt aat gaa cgg gtg cta gat gag gtg acc aat ggc aca gtg agt gtg 960
108 Ser Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val
109 305      310      315      320
111 tct aag gat ggc agt ctt ctt ttc cag cag gtg cag gtc gag gac ggt 1008
112 Ser Lys Asp Gly Ser Leu Leu Phe Gln Gln Val Gln Val Glu Asp Gly
113      325      330      335
115 ggt gtg tat acc tgc tat gcc atg gga gag act ttc aat gag aca ctg 1056
116 Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
117      340      345      350
119 tct gtg gaa ttg aaa gtg cac aat ttc acc ttg cac gga cac cat gac 1104
120 Ser Val Glu Leu Lys Val His Asn Phe Thr Leu His Gly His His Asp
121      355      360      365
123 acc ctc aac aca gcc tat acc acc cta gtg ggc tgt atc ctt agt gtg 1152
124 Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
125      370      375      380
127 gtc ctg gtc ctc ata tac cta tac ctc acc cct tgc cgc tgc tgg tgc 1200

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128 Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
129 385                      390                      395                      400
131 cgg ggt gta gag aag cct tcc agc cat caa gga gac agc ctc agc tct 1248
132 Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
133                      405                      410                      415
135 tcc atg ctt agt acc aca ccc aac cat gat cct atg gct ggt ggg gac 1296
136 Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
137                      420                      425                      430
139 aaa gat gat ggt ttt gac cgg cgg gtg gct ttc ctg gaa cct gct gga 1344
140 Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
141                      435                      440                      445
143 cct ggg cag ggt caa aac ggc aag ctc aag cca ggc aac acc ctg cca 1392
144 Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
145                      450                      455                      460
147 gtg cct gag gcc aca ggc aag ggc caa cgg agg atg tcg gat cca gaa 1440
148 Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
149 465                      470                      475                      480
151 tca gtc agc tcg gtc ttc tct gat acg ccc att gtg gtg 1479
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153                      485                      490
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157 <211> LENGTH: 493
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 2
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165 Leu Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val
166 20 25 30
168 Ser Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser
169 35 40 45
171 Lys Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala
172 50 55 60
174 Leu Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp
175 65 70 75 80
177 Thr Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn
178 85 90 95
180 His Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu
181 100 105 110
183 Arg Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe
184 115 120 125
186 Leu Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Leu Tyr Asn Asn
187 130 135 140
189 His Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu
190 145 150 155 160
192 Gln Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu
193 165 170 175
195 Leu Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu
196 180 185 190

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198 Ser Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu
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201 Pro Ala Trp Ile Lys Asn Gly Leu Tyr Leu His Asn Asn Pro Leu Asn
202          210          215          220
204 Cys Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln
205 225          230          235          240
207 Leu Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser
208          245          250          255
210 Lys Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu
211          260          265          270
213 Tyr Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile
214          275          280          285
216 Lys Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro
217          290          295          300
219 Ser Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val
220 305          310          315          320
222 Ser Lys Asp Gly Ser Leu Leu Phe Gln Gln Val Gln Val Glu Asp Gly
223          325          330          335
225 Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
226          340          345          350
228 Ser Val Glu Leu Lys Val His Asn Phe Thr Leu His Gly His His Asp
229          355          360          365
231 Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
232          370          375          380
234 Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
235 385          390          395          400
237 Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
238          405          410          415
240 Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
241          420          425          430
243 Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
244          435          440          445
246 Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
247          450          455          460
249 Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
250 465          470          475          480
252 Ser Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
253          485          490
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258 <211> LENGTH: 1566
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <220> FEATURE:
263 <221> NAME/KEY: CDS
264 <222> LOCATION: (1)..(1566)
266 <400> SEQUENCE: 3
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269 1 5 10 15

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271	aga	ccg	ggc	tgc	agg	gag	ctg	ctg	tgt	ttg	ctg	atg	atc	aca	gtg	act	96
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275	gtg	ggc	cct	ggt	gcc	tct	ggg	gtg	tgc	ccc	acc	gct	tgc	atc	tgt	gcc	144
276	Val	Gly	Pro	Gly	Ala	Ser	Gly	Val	Cys	Pro	Thr	Ala	Cys	Ile	Cys	Ala	
277			35					40					45				
279	act	gac	atc	gtc	agc	tgc	acc	aac	aaa	aac	ctg	tcc	aag	gtg	cct	ggg	192
280	Thr	Asp	Ile	Val	Ser	Cys	Thr	Asn	Lys	Asn	Leu	Ser	Lys	Val	Pro	Gly	
281			50					55					60				
283	aac	ctt	ttc	aga	ctg	att	aag	aga	ctg	gac	ctg	agt	tat	aac	aga	att	240
284	Asn	Leu	Phe	Arg	Leu	Ile	Lys	Arg	Leu	Asp	Leu	Ser	Tyr	Asn	Arg	Ile	
285			65					70					75			80	
287	ggg	ctt	ctg	gat	tct	gag	tgg	att	cca	gta	tcg	ttt	gca	aag	ctg	aac	288
288	Gly	Leu	Leu	Asp	Ser	Glu	Trp	Ile	Pro	Val	Ser	Phe	Ala	Lys	Leu	Asn	
289					85					90				95			
291	acc	cta	att	ctt	cgt	cat	aac	aac	atc	acc	agc	att	tcc	acg	ggc	agt	336
292	Thr	Leu	Ile	Leu	Arg	His	Asn	Asn	Ile	Thr	Ser	Ile	Ser	Thr	Gly	Ser	
293				100						105				110			
295	ttt	tcc	aca	act	cca	aat	ttg	aag	tgt	ctt	gac	tta	tcg	tcc	aat	aag	384
296	Phe	Ser	Thr	Thr	Pro	Asn	Leu	Lys	Cys	Leu	Asp	Leu	Ser	Ser	Asn	Lys	
297			115					120					125				
299	ctg	aag	acg	gtg	aaa	aat	gct	gta	ttc	caa	gag	ttg	aag	gtt	ctg	gaa	432
300	Leu	Lys	Thr	Val	Lys	Asn	Ala	Val	Phe	Gln	Glu	Leu	Lys	Val	Leu	Glu	
301			130					135					140				
303	gtg	ctt	ctg	ctt	tac	aac	aat	cac	ata	tcc	tat	ctc	gat	cct	tca	gcg	480
304	Val	Leu	Leu	Leu	Tyr	Asn	Asn	His	Ile	Ser	Tyr	Leu	Asp	Pro	Ser	Ala	
305			145					150					155			160	
307	ttt	gga	ggg	ctc	tcc	cag	ttg	cag	aaa	ctc	tac	tta	agt	gga	aat	ttt	528
308	Phe	Gly	Gly	Leu	Ser	Gln	Leu	Gln	Lys	Leu	Tyr	Leu	Ser	Gly	Asn	Phe	
309				165						170				175			
311	ctc	aca	cag	ttt	ccg	atg	gat	ttg	tat	gtt	gga	agg	ttc	aag	ctg	gca	576
312	Leu	Thr	Gln	Phe	Pro	Met	Asp	Leu	Tyr	Val	Gly	Arg	Phe	Lys	Leu	Ala	
313			180							185				190			
315	gaa	ctg	atg	ttt	tta	gat	gtt	tct	tat	aac	cga	att	cct	tcc	atg	cca	624
316	Glu	Leu	Met	Phe	Leu	Asp	Val	Ser	Tyr	Asn	Arg	Ile	Pro	Ser	Met	Pro	
317			195					200					205				
319	atg	cac	cac	ata	aat	tta	gtg	cca	gga	aaa	cag	ctg	aga	ggc	atc	tac	672
320	Met	His	His	Ile	Asn	Leu	Val	Pro	Gly	Lys	Gln	Leu	Arg	Gly	Ile	Tyr	
321			210					215					220				
323	ctt	cat	gga	aac	cca	ttt	gtc	tgt	gac	tgt	tcc	ctg	tac	tcc	ttg	ctg	720
324	Leu	His	Gly	Asn	Pro	Phe	Val	Cys	Asp	Cys	Ser	Leu	Tyr	Ser	Leu	Leu	
325			225					230					235			240	
327	gtc	ttt	tgg	tat	cgt	agg	cac	ttt	agc	tca	gtg	atg	gat	ttt	aag	aac	768
328	Val	Phe	Trp	Tyr	Arg	Arg	His	Phe	Ser	Ser	Val	Met	Asp	Phe	Lys	Asn	
329				245						250				255			
331	gat	tac	acc	tgt	cgc	ctg	tgg	tct	gac	tcc	agg	cac	tcg	cgt	cag	gta	816
332	Asp	Tyr	Thr	Cys	Arg	Leu	Trp	Ser	Asp	Ser	Arg	His	Ser	Arg	Gln	Val	
333			260						265					270			
335	ctt	ctg	ctc	cag	gat	agc	ttt	atg	aat	tgc	tct	gac	agc	atc	atc	aat	864

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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~~Seq#:39; Xaa Pos. 86,87,88,89,90,91,93,94,96,97,98,100,102,104,105,107,109~~
~~Seq#:39; Xaa Pos. 110,111,112,113,114,115,117,118,120,121,123,124,126,128~~
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Seq#:40; Xaa Pos. 1,4,6,8,9,11,14,15,16,18,19,21,22,23,25,26,27,28
Seq#:41; Xaa Pos. 1,3,6,8,9,11,15,17,18,19,20,21,22,23,25,26,28,29
Seq#:79; Xaa Pos. 2,3,5,7,8,10,11,12,13,14,15,16,17,18,19

VERIFICATION SUMMARY

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L:6144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:6148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:16
L:6152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:32
L:6156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:48
L:6160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:64
L:6164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:80
L:6168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:96
L:6172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:112
L:6176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:128
L:6242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:6246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:16
L:6311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:6315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:16
L:6820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:6824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:16